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EXAMINER	
WONG, LESLIE	
ART UNIT	**PAPER NUMBER**
2177	

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/865,090	GARNER ET AL.	
	Examiner	Art Unit	
	Leslie Wong	2177	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *10 May 2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-24* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-24* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Response to Request for Reconsideration

1. Receipt of Applicant's Request for Reconsideration, filed 10 May 2004, is acknowledged.

Claim Rejections - 35 USC § 103

2. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

3. Claims 1, 3, 6, and 8-24 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis).

Regarding claims 1, 13, and 17, **Wolffe** teach computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding annotations, the system comprising:

a). a search function which searches the annotations of the dataset according to a user defined criterion and outputs a first subset of the dataset restricted by the criterion (¶s 0397, 0398).

c). a selection function which applies to the second subset a user-defined selection parameter and outputs a third subset restricted relative to the second subset by the parameter (¶s 358, 386) .

d). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset (¶s 350, 391, 392).

b). **Wolffe** does not explicitly teach a redundancy reducing function which compares the first subset with a first database correlating the sequence identifiers of the first subset with syngeneic biopolymers and outputs a second subset of the dataset

having **reduced unique**, natural complex biopolymer **redundancy** relative to the first subset.

Hennig, however, teaches a redundancy reducing function which compares the first subset with a first database correlating the sequence identifiers of the first subset with syngeneic biopolymers and outputs a second subset of the dataset having reduced unique, natural complex biopolymer redundancy relative to the first subset (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Hennig's** teaching would have allowed **Wolffe's** to clean, remove duplicates, and perform quality checks to the raw sequence in preparation for the sequence comparative analysis as indicated in Section 1 – Introduction, lines 1-11 and Section 2.2. Image Analysis, last paragraph.

Regarding claims 3 and 6, **Wolffe** further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria (¶s 0397, 0398).

Regarding claims 8 and 11, **Hennig** further teach wherein the database is one of a plurality of databases correlating the sequence identifiers of the first subset with

syngeneic biopolymers, and the redundancy reducing function compares the first subset with the databases and outputs the second subset of the dataset (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

Regarding claims 9 and 16, **Wolffe** further teach wherein the parameter is selected from the group consisting of source (i.e., Genbank), species, author, and pathway (¶s 002, 99, 234).

Regarding claim 10, **Wolffe** further teach wherein the parameter is one of a plurality of user-defined selection parameters, and the selection function applies to the second subset the parameters and outputs the third subset restricted relative to the second subset by the parameters (¶s 0397, 0398).

Regarding claim 12, **Wolffe** further teach comprising an expansion function which searches a second database for synonyms of the sequence identifiers of the first, second or third subset (¶s 0132, 0133).

Regarding claim 19, **Wolffe** further teach wherein the second annotations comprise data attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset, said data selected from the group consisting of:

gene expression data, sequencing data, genotype data, polymorphism data and clinical data (¶s 0006, 0031, 0083, 299, and 0322).

Regarding claims 14, 15, 18, 20, 21, 22, and 23, **Wolffe** further teach steps of:

b). a tabulation function which crates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset (¶s 350, 391, 392).

c). a third computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding first annotations, the third system comprising:

1). an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which link, the second annotations to the corresponding sequence identifiers of the subset (¶s 0038-0042; 344); and

2). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations (¶s 350, 391, 392).

a). **Wolffe** does not explicitly teach a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer **redundancy** relative to the sum.

Hennig, however, teaches a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer **redundancy** relative to the sum (Section 2.5.1 Cleaning of raw sequence data; Section 1. Introduction, lines 1-4, and Section 2.2. Image Analysis, last paragraph).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Hennig's** teaching would have allowed **Wolffe's** to clean, remove duplicates, and perform quality checks to the raw sequence in preparation for the sequence comparative analysis as indicated in Section 1 – Introduction, lines 1-11 and Section 2.2. Image Analysis, last paragraph.

Regarding claim 24, **Wolffe** further teach wherein the system is ARROGANT (¶ 0012). The cited portion facilitates identification, analysis, and comparison of collections of genes and clones. Therefore, it is equivalent to the ARROGANT system.

4. Claims 2 and 4 are rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **Lincoln et al. "Lincoln"** (U.S. Patent 6,303,297).

Regarding claim 2, **Wolffe** and **Hennig** do not explicitly teach wherein the criterion is selected from the group consisting of a keyword and a concept.

Lincoln, however, teaches wherein the criterion is selected from the group consisting of a keyword and a concept (col. 20, lines 38-50).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Lincoln's** teaching would have allowed **Wolffe** and **Hennig's** the ability to access genetic information to perform comparative analysis in a more effective manner as users can enter a search concept via keywords as disclosed in col. 20, lines 38-44.

Regarding claim 4, **Wolffe** further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria (¶s 0397, 0398).

Wolffe and **Hennig** do not explicitly teach wherein the criteria include multiple keywords.

Lincoln, however, teaches wherein the criteria include multiple keywords (col. 20, lines 42-44).

5. Claim 5 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **Chin et al.** (U.S. Patent 6,470,277).

Regarding claim 5, **Wolffe** further teach wherein the dataset is selected from GenBank (¶ 0348).

Wolffe and **Hennig** do not explicitly do not explicitly teach wherein the dataset is selected from the group consisting GenBank, Medline, and KEGG.

Chin et al., however, teach wherein the dataset is selected from the group consisting Medline and KEGG (col. 11, lines 29-46; col. 18, lines 54-59).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Chin's** teaching would have allowed **Wolffe** and **Hennig's** to include Medline and KEGG for sequence searching because these databases contain functional information related to known genes and would be helpful for researchers to be able to access the mentioned databases.

6. Claim 7 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Wolffe et al. "Wolffe"** (US 2002/0081603 A1) and in view of **Hennig et al. "Hennig"** (A data-analysis pipeline for large-scale gene expression analysis) as applied to claims 1, 3, 6, and 8-24 above, and further in view of **MacLeod et al.** (U.S. Patent 6,221,600 B1).

Regarding claim 7, **Wolffe** does not explicitly teach wherein the database is selected from the group consisting of UniGene and LocusLink.

Hennig teaches wherein the database is selected from the group consisting of Genbank, Swissprot+Tremble, Unigene, dbEst, GeneCards, and a lab-internal EST database (Section 2.5.2 Data base mining and handling of results, first paragraph).

Wolffe and **Hennig** do not explicitly teach wherein the database is selected from the group consisting of LocusLink.

MacLeod et al., however, teach wherein the database is selected from the group consisting of UniGene and LocusLink (col. 13, lines 43-58).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine the teachings of the cited references because **Chin's** teaching would have allowed **Wolffe** and **Hennig's** users to have access to UniGene and LocusLink to search and create collections of sequences as this would provide various of sources for users to search, extract, and manipulate the information.

Response to Argument

7. Applicant's arguments filed 10 May 2004 have been fully considered but they are not persuasive.

Applicants argue that Wolffe protocol is neither applicable nor germane to the field of their invention as Wolffe identifies accessible genomic sequences and characterizes them as regulatory sequences using known alignment algorithms while Applicants' invention a protocol for generating targeted collections of sequences from a dataset of sequence identifier corresponding to natural complex biopolymer sequences and liked to corresponding annotations. In response to the preceding arguments, Examiner respectfully submits that Wolffe teaches identification, isolation, and characterization of regulatory DNA sequences in a cell of interest. Also, Wolffe provides libraries of regulatory sequences and utilizing the databases to conduct various genetic analysis, and uses of accessible regulatory sequences in the design of vectors bearing transgenes (abstract). Wolffe also teaches expressed genes (i.e., EST) analysis and computerized analysis of a genome sequences by comparison to databases of expressed sequence tags (¶0006). Further, Wolffe teaches the sequence(s) to be compared against a comparison sequence is (are) typically obtained from an internal database populated as set forth supra, but can also be obtained from an external database. In general, an external database refers to a database that is located outside of the internal database. Examples of external databases include GenBank and other associated databases that are maintained by the National Center

for Biotechnology Information (NCBI), part of the National Library of Medicine. The comparison or reference sequences can be stored with the sequences being compared on the internal database or can be stored in a separate database that is either another internal database or an external database (¶348). Applicants' abstract discloses methods for the design, comparison and analysis of genetic and proteomic databases and that it uses ARROGANT to make annotation for a large assembly of genes makes the collection of genomic/EST sequences truly informative. Examiner submits that Wolffe teaches relevant subject matter to Applicants' claim invention and that the prior art is applicable to Applicants' invention as it teaches comparison and analysis of sequences as mentioned above.

Applicants argue that how does the practitioner of Wolffe find applicable relevance in Hennig, and to what end? Wolffe is characterizing novel regulatory sequences by using alignment tools to compare them with known sequences. Henning is characterizing large EST libraries based on oligo fingerprinting so as to reduce the number of clones that need to be sequenced. In response to the preceding arguments, Examiner respectfully submits that Wolffe utilizes Genbank and NCBI as external databases to search and retrieve desired genes/sequences information for comparison and analysis. Hennig also uses NCBI to obtain its genes/sequences information for gene expression analysis. Hennig teaches that the goal of most large-scale EST projects is the **generation of a unique set of sequences** (page 165, Introduction section, lines 1-2) and that the database of expressed sequence tags (dbEST)

maintained at the NCBI comprises around 1.6 million human EST sequences is **highly redundant** (page 165, Introduction section, lines 5-11). Applicants' Specification page 11, lines 3-26 discloses that the redundancy reducing function outputs a second subset of the dataset having *reduced unique*, natural complex biopolymer redundancy relative to the first subset by comparing the first subset with a first database correlating the sequence identifiers of the first subset with syngeneic biopolymers and outputs a second subset of the dataset having reduced unique, natural complex biopolymer redundancy relative to the first subset. Wolffe performs comparison by comparing the comparison sequences and the reference sequences. Wolffe further teaches that the comparison sequences can be obtained from external databases such as NCBI. As mentioned above Hennig recognizes that NCBI is highly redundant database, thus, one of the ordinary skill in the art would have been motivated to combine Wolffe and Hennig to obtain the **unique** set of sequences as suggested by Hennig at page 165, introduction lines 1-2.

Applicants argue that Applicants' claim must be read as a whole, as a system of specifically interrelated elements and that they donot claim any combination of database search, redundancy reducing, selection and tabulation functions. In response to the preceding arguments, Examiner respectfully submits that one of the ordinary skill in the art would have been motivated to insert an improvement such as the reduce redundancy step at any points in the claim in an effort to provide a more efficient

methodology for complex sequence analysis by cleaning and reducing redundancy to the sequences in order to make a dataset unique.

Applicants argue that the Action supplements Wolffe and Henning with several additional references: Lincoln, Chin, and MacLeod. No amount of alchemy is going to alter the subject mater Wolffe, and these additional references do not add relevant content to the already cited art. Examiner respectfully submits Lincoln, Chin, and MacLeod are all relevant prior arts as they teach similar subject matters to Applicant's claimed invention. Chin teaches techniques for facilitating the identification of **candidate genes for a plurality of DNA sequences** (abstract lines 1-2), Lincoln teaches database storage and retrieval system for genetic information and related annotated information and **analysis of full-length sequences** (abstract). Finally, MacLeod teaches detection of **gene expression and analysis** of both known and unknown genes.

Conclusion

8. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

Fleischmann et al. (U.S. Patent 6,355,450 B1).

Nadimpalli et al. (U.S. Patent 6,421,613 B1).

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Leslie Wong whose telephone number is (703) 305-3018. The examiner can normally be reached on Monday to Friday 9:30am - 6:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John E Breene can be reached on (703) 305-9790. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Leslie Wong
Patent Examiner
Art Unit 2177

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July 22, 2004

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